Raw Sequence Listing

09/12/91 13:15:19

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1
   WPC(
2
7
8
  (1)ê
9
10
11
12
13
          1) This does not appear to be
14
15
              in ASCII text
16
17
           2) No "General Information" has
18
19
              been included, which is mandatory.
20
21
              Please See attached sample
22
23
              OF what the Sequencer Listing should
24
25
              look like.
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54	
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56	
57	ê
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59	ê
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62	ê
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64	
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66	ê
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68	ê
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71	ê
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73	
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75	ê
76	
77	ê
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80	ê
81	·
82	
83	ê
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87	ê
88	6
89	a
90	e
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92	ê
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96	а
97	/0.0
98	(2)ê
99	•
100	ê
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102	ê
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104	•
105	ê
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107
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118
119 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG ê
120 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTTê
121 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAGê
122 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTCê
123 CCCCCTCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTATê
124
    AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGTê
125
    126
    TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CCê
127
128
    (2)ê
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147
    ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT ê
148
    Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
149
                      5
                                        10
150
    GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAAê
151
    Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
152
                 20
                                    25
                                                       30
153
    GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA ê
    Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
155
             35
                                40
    AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG
156
                                                                       192
157
    Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
158
                             55
                                                60
159
    TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC
                                                                       240
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160 161		Glu	Arg	Asp	Val	Ala	Trp	Ile	Ala	Arg		Ser	Lys	Arg	Met	Ser 80	
162	65 mcm	C/II/C	C 3 (7)	030	CAM	70 GAA	C 3 C	OBM	010	O B ID	75	030	C B ID	030	ma a		200
163																	288
164	261	AHT	Asp	GIU		Glu	Asp	Asp	GIU		ASP	GIU	Asp	Asp	95	TYF	
165	030	C 7 C	C 3 C	030	85	030	030	0 B ID	000	90	mam	a s m	03m	030		03 m	226
						GAC											336
166	Asp	Asp	GIU		Asp	Asp	Asp	Asp		Pne	туг	Asp	Asp		Asp	Asp	
167				100					105					110			204
168						GAG											384
169	GIU	GIU		GIU	Leu	Glu	Asn		Met	Asp	Asp	GIU		GIU	Asp	Glu	
170			115					120					125				400
171						AGC							-				432
172	Ala		GIu	GIu	Met	Ser		GIu	Met	GTĀ	Ala		Ala	Glu	Glu	Met	
173		130					135					140					
174	_					TGT											480
175		Ala	GTĀ	Ala	Asn	Cys	Ala	Cys	Val	Pro		His	His	Leu	Arg	-	
176	145					150					155					160	
177						AGG			-								528
178	Asn	Glu	Val	Lys	_	Arg	Met	Ile	Tyr		Phe	His	Asp	Pro		Phe	
179					165					170					175		
180						GTG											576
181	Leu	Val	Ser		Pro	Val	Asn	Pro		Glu	Gln	Met	Glu		Arg	Cys	
182				180					185					190			
183						GAG											624
184	Glu	Asn		Asp	Glu	Glu	Val		Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
185			195					200				210					
186	GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	TTC	TCA	CCT	672
187	Glu	_				Glu											672
187 188	_	_															672
187	Glu	_				Glu					Pro					Pro	672
187 188 189 190	Glu 220 TAG	Glu				Glu					Pro					Pro	672 675å
187 188 189 190 191	Glu 220	Glu				Glu					Pro					Pro	
187 188 189 190 191	Glu 220 TAG	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193	Glu 220 TAG	Glu				Glu					Pro					Pro	
187 188 189 190 191	Glu 220 TAG (2) é	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193	Glu 220 TAG (2) é	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193 194 195	Glu 220 TAG (2) é	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193 194 195 196	Glu 220 TAG (2) é ê	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197	Glu 220 TAG (2) é	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198	Glu 220 TAG (2) é ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200	Glu 220 TAG (2) é ê ê	Glu				Glu					Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	Glu 220 TAG (2) é ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	
187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208	Glu 220 TAG (2) é ê ê	Glu				Glu		Met			Pro					Pro	

Raw Sequence Listing

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TTCCCCTTCA TTAATTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT
                                                                       120
213
    TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC
                                                                       180
    ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC
215
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    ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT
241
    GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT
242
    CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG
243
    AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT
244
    CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA
245
    CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT
246 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG
247
    CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG
248
    CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT
249
    ACCCTTTGTG CC
250 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA
251
    GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG
252
    TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC
    TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC
254
    ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC
255
    TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG
256
    GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC
257
    GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT
258
    GAG GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA
259
    GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA
260
    GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT
    261
262
    TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG
263
    AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT
    GAA GAG GTT GCA ATG GAA GAA GAA GAA GAA GAG GAG GAG
265
    GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT
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266
     TAG
267
     GCATGCAGTT GCAAAGCCCA GAAGAAGAA ATGGACAGCG GAAGAAGTGG
268
     TTGTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA
269
270
     ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT
271
     CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT
272
     GTTAAAAATA AAAGTTTGAC TTGCATAC ê
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296
    ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT ê
     GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT ê
297
298
     CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG ê
299
     AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT ê
300
    CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA ê
301
     CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT ê
302
    AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG ê
303
     CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG ê
304
     CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT ê
305
    ACCCTTTGTG CC ê
306
    ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA ê
307
    GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG ê
308
    TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC ê
309
    TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC ê
310
    ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC ê
311
    TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG ê
312
    GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC ê
313
    GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT ê
314
    GAG GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA ê
315
    GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA ê
316
    GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T ê
317
    GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA ê
318
    CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC ê
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319
    TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC ê
320
    CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC ê
     TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC ê
321
322
     TCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC ê
323
     TTCAGGCTTC CCCATTTGCT CCTCTCCGA AACCCTCCCC TTCCTGTTCC ê
324
     CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT ê
325
     TCACCAGCTT TGCTCTCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT ê
326
    TCCTGCTCCC CTCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT ê
327
     CTACCTGCTT CCCTCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG ê
328
     TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT ê
329
     CCTCCCTCCC CCTCCCAGG CCTTTTTTT TTTTTTTTT TTTTTTTTT ê
330
     TTGGTTTTC GAGACAGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC ê
     TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG ê
331
332
     CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG ê
333
     GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT ê
334
    AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT ê
335
     TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC ê
     CCTCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT ê
336
337
     GCCCCGTTCC CCTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC ê
338
339
340
    AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT ê
341
    TTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCC TCCGGCTTCC ê
342
     343
    TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT ê
344
     CTTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT ê
     CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC ê
346
    CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTGT TTCTCCCACT ê
    TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG ê
347
348
    GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC ê
349
     CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT ê
350
    ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT ê
351
    CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTCCA TTTTCTTCCA ê
     CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT ê
353
    TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC ê
354
    ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC ê
355
    TTCCCTTTGC TTCTCCCTC TCCTTTCCCC TTCCCCTATG CCCTCTACTC ê
356
    TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC ê
357
     CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC ê
358
    ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA ê
    AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC ê
360
    AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT ê
361
    CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG ê
362
    CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA ê
363
    GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG ê
364
    TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA ê
365
    TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA ê
366
    GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT â
367
    TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG ê
368
     GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT ê
369
    AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ê
370
    ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA ê
371
    AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA Â
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372 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC ê
373 TTC TCA CCT TAG ê
374 GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA ê
375
    GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA ê
376
    TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA ê
377
     CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT ê
    GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA ê
378
379
     GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG ê
380
    TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT ê
    TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG ê
381
382
     TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT ê
    CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT ê
383
384
     TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA ê
385 AATGTTTTT AAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA ê
386
    GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA ê
387
     GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC ê
388 CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ê
389
     ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ê
390
    ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA ê
391
392 AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC ê
393
    AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT ê
394 TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA ê
395
    TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT ê
396
     GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA ê
     AATAAAAGTT TGACTTGCAT AC ê
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419
    Leu Leu His Arg Tyr Ser Leu Glu Glu Ile Leu Pro Tyr Leu Gly Trp
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421
    Val Phe Ala Val Val Thr Thr Ser Phe
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446
      GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG ê
447
      GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC ê
448
      TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG ê
449
      GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT ê
450
      TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT ê
451
      GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA ê
452
      CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT ê
453
      CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC ê
454
      TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC ê
455
      CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA_GATCTGTAAG TAGGCCTTTG ê
456
      TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT ê
457
      CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT ê
458
      GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC ê
459
      ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG ê
460
      GTGTGTGTGC AGGCTGCCAC CTCCTCCTC TCTCCTCTGG TCCTGGGCAC ê
461
      CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC ê
     AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA ê
462
463
      CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG ê
464
      TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT ê
465
      TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG ê
466
      GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA ê
467
     GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG ê
468
      TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA ê
      GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC ê
469
470
      AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG ê
471
     CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT ê
      GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA ê
472
473
      TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC ê
474
     CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT ê
475
     ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT ê
476
      TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT ê
477
      CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC ê
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Raw Sequence Listing

09/12/91 13:15:59

TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG ARA ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC GTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG ARA GATTTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC AGCATCTGC TTTTTGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG							
TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT TCAAATGTTT TTTTTTAAGG GATGGTTGAA TGAACTTCAG CATCCAAGTT TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA AS3 GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG A84 ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA AS5 AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC A86 CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG A87 AATTCTTCCT GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG A89 AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC A90 TTTTTGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT A91 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG A92 AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA A93 GGGTGTGGG CTCCGGGTGA GAGTGGTGGA-GTGTCAATGC CCTGAGCTGG A94 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	478	ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	ê
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491 CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG 492 AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA 493 GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA-GTGTCAATGC CCTGAGCTGG 494 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	489	AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	ê
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493 GGGTGTGGG CTCCGGGTGA GAGTGGTGGA-GTGTCAATGC CCTGAGCTGG 494 GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	491	CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	ê
494 GGCATTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT	492	AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	ê
	493	GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	-GTGTCAATGC	CCTGAGCTGG	ê
495 AATGATCTTG GGTGGATCC ê	494	GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	ê
	495	AATGATCTTG	GGTGGATCC	ê			

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/728,838 DATE: 09/12/91 TIME: 13:16:00

LINE ERROR ORIGINAL TEXT

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8	Unknown or Misplaced Identifier	(1)A
11	Unknown or Misplaced Identifier	A
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113	Unknown or Misplaced Identifier	A
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120	Unknown or Misplaced Identifier	ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATC
121	Unknown or Misplaced Identifier	CTCGTGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTT
122	Unknown or Misplaced Identifier	CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTC
123	Unknown or Misplaced Identifier	CCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTC
124	Unknown or Misplaced Identifier	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCC
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126	Unknown or Misplaced Identifier	
127	Unknown or Misplaced Identifier	TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTT
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SEQUENCE VERIFICATION REPORT DATE: 09/12/91 PATENT APPLICATION US/07/728,838 TIME: 13:16:00

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147	Unknown or Misplaced Identifi	er	ATG 3	TCT	GAT	AAC	AAG	AAA	CCA	GAC	AAA	GCC
148	Unknown or Misplaced Identifi	er	Met S	Ser	Asp	Asn	Lys	Lys	Pro	Asp	Lys	Ala
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151	Unknown or Misplaced Identifi	er	Asp (Gly	Asp	Gly	Asn	Arg	Cys	Asn	Leu	Leu
152	Unknown or Misplaced Identifi		20	-	-	•		25	-			
153	Unknown or Misplaced Identifi		GAA A	ATT	CTG	CCT	TAT	CTA	GGG	TGG	CTG	GTC
154	Unknown or Misplaced Identifi		Glu 1									
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169	Unknown or Misplaced Identifi		Glu (
170	Unknown or Misplaced Identifi		115	JLU	GIU	GIU	Leu	120	ASH	Lou	Mec	vob
171	Unknown or Misplaced Identifi		GCC (222	CAA	GNG	ATC.		ста	GNN	ATG	CCT
172	Unknown or Misplaced Identifi		Ala (
173	Unknown or Misplaced Identifi		130	JIU	GIU	GIU	Mel	135	VAI	GIU	Mec	GIY
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185	Unknown or Misplaced Identifi		Glu A	ASH	WIR	Asp	GIU		VAI	ATA	Met	
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			HILLOUDDI AUNOVIOLA VIIGIA

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/728,838

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DATE: 09/12/91 TIME: 13:16:00

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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/728,838

DATE: 09/12/91 TIME: 13:16:00

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SEQUENCE VERIFICATION REPORT DATE: 09/12/91 PATENT APPLICATION US/07/728,838 TIME: 13:16:00

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PAGE: 7

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/07/728,838

DATE: 09/12/91 TIME: 13:16:00

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Felfe and Lynch 805 Third Avenue New York, NY 10022

Thierry,Boon 07/728,838 July 9, 1991

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES Mailed: 9 / 9 / 9 /
This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:
1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of \$\ 1.821 \text{ through } 1.825 \text{ as follows:}
a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically:
b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically:
d. Other:
5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically:
8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically:
11. Other:
APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE ABOVE REQUIREMENTS. Failure to comply with the above requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR § 1.136. Direct the response to, and any questions about, this notice to the undersigned. A copy of this notice MUST be returned with your response.
For: Manager, Application Processing Division Examining Group

Felfe and Lynch 805 Third Avenue New York, NY 10022

Thierry Boon 07/728,838 July 9, 1991

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES
This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:
1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of \$\ \frac{1}{2} \f
a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically:
b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically:
d. Other:
5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically: The infanction is not in Ascar front.
8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically:
readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically:
to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in companied by a statement that the substitute data is identical to that originally